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Betzner, Andreas
Freyssinet, Georges
Perez, Pascal

<120> METHOD FOR OBTAINING PLANT VARIETIES

<130> A33153-PCT-USA 072667.0128

<140> 09/529,239

<141> 2000-10-27

<150> PCT/EP98/06977

<151> 1998-10-09

<160> 100

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<223> Degenerate oligonucleotides UPMU used to isolate
AtMSH3 and AtMSH6.

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<301> Reenan and Kolodner

<302> Genetics

<303> 132

<306> 963-973

<307> 1992

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<223> Degenerate oligonucleotides DOMU used to isolate
AtMSH3 and AtMSH6.

<221> modified_base

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<210> 3

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<223> MSH3 specific primer 636 for PCR using cDNA of
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24

<210> 4

<211> 27

<212> DNA

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<220>

<223> Primer AP1 for PCR using cDNA of Arabidopsis
thaliana ecotype Columbia containing adapter
sequences ligated to both its ends.

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27

<210> 5

<211> 23

<212> DNA

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<223> Primer AP2 for PCR using cDNA of Arabidopsis
thaliana ecotype Columbia containing adapter
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 Arabidopsis thaliana ecotype Columbia.

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 <210> 7
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 <223> MSH3 specific primer S51 for PCR using cDNA of
 Arabidopsis thaliana ecotype Columbia.

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 <210> 8
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 <210> 9
 <211> 28
 <212> DNA
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 <223> MSH3 specific primer S523 for PCR using cDNA of
 Arabidopsis thaliana ecotype Columbia.

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 <210> 10
 <211> 33
 <212> DNA
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<223> MSH3 specific primer 1S5 for PCR using cDNA of
Arabidopsis thaliana ecotype Columbia.

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33

<210> 11

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<223> MSH3 specific primer S53 for PCR using cDNA of
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<210> 12

<211> 1250

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<211> 34

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34

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> MSH3 specific primer S52 for PCR using cDNA of Arabidopsis thaliana ecotype Columbia.

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<210> 15

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<212> DNA

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<221> misc_feature

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tctctcagcc aatactctgc aacagttgga ggttgtgaaa aataattcag atggatcgga 180
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<210> 16
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<213> Artificial Sequence

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<220>
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        Arabidopsis thaliana ecotype Columbia.

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<210> 17
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> MSH3 specific primer S525 for PCR using cDNA of
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<210> 18
<211> 3522
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<213> Arabidopsis thaliana ecotype Columbia

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<222> (100)...(3342)
<223> AtMSH3 full-length cDNA and deduced sequence of
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                                     Met Gly Lys Gln Lys
                                     1         5

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cag cag acg att tet cgt ttc ttc gct ccc aaa ccc aaa tcc ccg act    162
Gln Gln Thr Ile Ser Arg Phe Phe Ala Pro Lys Pro Lys Ser Pro Thr
          10              15              20

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cac gaa ccg aat ccg gta gcc gaa tca tca aca ccg cca ccg aag ata    210
His Glu Pro Asn Pro Val Ala Glu Ser Ser Thr Pro Pro Pro Lys Ile
          25              30              35

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tcc gcc act gta tcc ttc tct cct tcc aag cgt aag ctt ctc tcc gac	258
Ser Ala Thr Val Ser Phe Ser Pro Ser Lys Arg Lys Leu Leu Ser Asp	
40 45 50	
cac ctc gcc gcc gcg tca ccc aaa aag cct aaa ctt tct cct cac act	306
His Leu Ala Ala Ala Ser Pro Lys Lys Pro Lys Leu Ser Pro His Thr	
55 60 65	
caa aac cca gta ccc gat ccc aat tta cac caa aga ttt ctc cag aga	354
Gln Asn Pro Val Pro Asp Pro Asn Leu His Gln Arg Phe Leu Gln Arg	
70 75 80 85	
ttt ctg gaa ccc tcg ccg gag gaa tat gtt ccc gaa acg tca tca tcg	402
Phe Leu Glu Pro Ser Pro Glu Glu Tyr Val Pro Glu Thr Ser Ser Ser	
90 95 100	
agg aaa tac aca cca ttg gaa cag caa gtg gtg gag cta aag agc aag	450
Arg Lys Tyr Thr Pro Leu Glu Gln Gln Val Val Glu Leu Lys Ser Lys	
105 110 115	
tac cca gat gtg gtt ttg atg gtg gaa gtt ggt tac agg tac aga ttc	498
Tyr Pro Asp Val Val Leu Met Val Glu Val Gly Tyr Arg Tyr Arg Phe	
120 125 130	
ttc gga gaa gac gcg gag atc gca gca cgc gtg ttg ggt att tac gct	546
Phe Gly Glu Asp Ala Glu Ile Ala Ala Arg Val Leu Gly Ile Tyr Ala	
135 140 145	
cat atg gat cac aat ttc atg acg gcg agt gtg cca aca ttt cga ttg	594
His Met Asp His Asn Phe Met Thr Ala Ser Val Pro Thr Phe Arg Leu	
150 155 160 165	
aat ttc cat gtg aga aga ctg gtg aat gca gga tac aag att ggt gta	642
Asn Phe His Val Arg Arg Leu Val Asn Ala Gly Tyr Lys Ile Gly Val	
170 175 180	
gtg aag cag act gaa act gca gcc att aag tcc cat ggt gca aac cgg	690
Val Lys Gln Thr Glu Thr Ala Ala Ile Lys Ser His Gly Ala Asn Arg	
185 190 195	
acc ggc cct ttt ttc cgg gga ctg tcg gcg ttg tat acc aaa gcc acg	738
Thr Gly Pro Phe Phe Arg Gly Leu Ser Ala Leu Tyr Thr Lys Ala Thr	
200 205 210	
ctt gaa gcg gct gag gat ata agt ggt ggt tgt ggt ggt gaa gaa ggt	786
Leu Glu Ala Ala Glu Asp Ile Ser Gly Gly Cys Gly Gly Glu Glu Gly	
215 220 225	
ttt ggt tca cag agt aat ttc ttg gtt tgt gtt gtg gat gag aga gtt	834
Phe Gly Ser Gln Ser Asn Phe Leu Val Cys Val Val Asp Glu Arg Val	
230 235 240 245	
aag tcg gag aca tta ggc tgt ggt att gaa atg agt ttt gat gtt aga	882
Lys Ser Glu Thr Leu Gly Cys Gly Ile Glu Met Ser Phe Asp Val Arg	
250 255 260	

gtc ggt gtt gtt ggc gtt gaa att tcg aca ggt gaa gtt gtt tat gaa	930
Val Gly Val Val Gly Val Glu Ile Ser Thr Gly Glu Val Val Tyr Glu	
265 270 275	
gag ttc aat gat aat ttc atg aga agt gga tta gag gct gtg att ttg	978
Glu Phe Asn Asp Asn Phe Met Arg Ser Gly Leu Glu Ala Val Ile Leu	
280 285 290	
agc ttg tca cca gct gag ctg ttg ctt ggc cag cct ctt tca caa caa	1026
Ser Leu Ser Pro Ala Glu Leu Leu Leu Gly Gln Pro Leu Ser Gln Gln	
295 300 305	
act gag aag ttt ttg gtg gca cat gct gga cct acc tca aac gtt cga	1074
Thr Glu Lys Phe Leu Val Ala His Ala Gly Pro Thr Ser Asn Val Arg	
310 315 320 325	
gtg gaa cgt gcc tca ctg gat tgt ttc agc aat ggt aat gca gta gat	1122
Val Glu Arg Ala Ser Leu Asp Cys Phe Ser Asn Gly Asn Ala Val Asp	
330 335 340	
gag gtt att tca tta tgt gaa aaa atc agc gca ggt aac tta gaa gat	1170
Glu Val Ile Ser Leu Cys Glu Lys Ile Ser Ala Gly Asn Leu Glu Asp	
345 350 355	
gat aaa gaa atg aag ctg gag gct gct gaa aaa gga atg tct tgc ttg	1218
Asp Lys Glu Met Lys Leu Glu Ala Ala Glu Lys Gly Met Ser Cys Leu	
360 365 370	
aca gtt cat aca att atg aac atg cca cat ctg act gtt caa gcc ctc	1266
Thr Val His Thr Ile Met Asn Met Pro His Leu Thr Val Gln Ala Leu	
375 380 385	
gcc cta acg ttt tgc cat ctc aaa cag ttt gga ttt gaa agg atc ctt	1314
Ala Leu Thr Phe Cys His Leu Lys Gln Phe Gly Phe Glu Arg Ile Leu	
390 395 400 405	
tac caa ggg gcc tca ttt cgc tct ttg tca agt aac aca gag atg act	1362
Tyr Gln Gly Ala Ser Phe Arg Ser Leu Ser Asn Thr Glu Met Thr	
410 415 420	
ctc tca gcc aat act ctg caa cag ttg gag gtt gtg aaa aat aat tca	1410
Leu Ser Ala Asn Thr Leu Gln Gln Leu Glu Val Val Lys Asn Asn Ser	
425 430 435	
gat gga tcg gaa tct ggc tcc tta ttc cat aat atg aat cac aca ctt	1458
Asp Gly Ser Glu Ser Gly Ser Leu Phe His Asn Met Asn His Thr Leu	
440 445 450	
aca gta tat gct tcc agg ctt ctt aga cac tgg gtg act cat cct cta	1506
Thr Val Tyr Ala Ser Arg Leu Leu Arg His Trp Val Thr His Pro Leu	
455 460 465	
tgc gat aga aat ttg ata tct gct cgg ctt gat gct gtt tct gag att	1554
Cys Asp Arg Asn Leu Ile Ser Ala Arg Leu Asp Ala Val Ser Glu Ile	
470 475 480 485	
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gtg	ctc	tcc	tca	gtc	ttg	aca	gct	atg	tct	aga	tca	tct	gat	att	caa	1698	
Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg	Ser	Ser	Asp	Ile	Gln		
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cgt	gga	ata	aca	aga	atc	ttt	cat	cgg	act	gct	aaa	gcc	aca	gag	ttc	1746	
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Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly	Lys	Gln	Ile	Gln	Arg		
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Leu	Gly	Ile	Lys	Gln	Asp	Ser	Glu	Met	Arg	Ser	Met	Gln	Ser	Ala	Thr		
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Val	Arg	Ser	Thr	Leu	Leu	Arg	Lys	Leu	Ile	Ser	Val	Ile	Ser	Ser	Pro		
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gcg	gct	gtt	cga	ggg	gac	ttg	ctc	gac	ata	cta	atc	act	tcc	agc	gac	1986	
Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu	Ile	Thr	Ser	Ser	Asp		
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Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala	Val	Leu	Val	Ile	Arg		
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gaa	aag	ctg	gat	tcc	tcg	ata	gct	tca	ttt	cgc	aag	aag	ctc	gct	att	2082	
Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg	Lys	Lys	Leu	Ala	Ile		
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cga	aat	ttg	gaa	ttt	ctt	caa	gtg	tcg	ggg	atc	aca	cat	ttg	ata	gag	2130	
Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile	Thr	His	Leu	Ile	Glu		
							665								675		
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Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	Met	Asn	Trp	Val	Lys	Val	Asn	Ser		
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gat	gag	cta	gct	cta	gca	act	gaa	cat	ctt	gcc	att	gtg	aac	cga	gct	2274	
Asp	Glu	Leu	Ala	Leu	Ala	Thr	Glu	His	Leu	Ala	Ile	Val	Asn	Arg	Ala		

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tcg tgg gat agt ttc ctc aag agt ttc agt aga tac tac aca gat ttt				2322
Ser Trp Asp Ser Phe Leu Lys Ser Phe Ser Arg Tyr Tyr Thr Asp Phe	730	735	740	
aag gct gcc gtt caa gct ctt gct gca ctg gac tgt ttg cac tcc ctt				2370
Lys Ala Ala Val Gln Ala Leu Ala Leu Asp Cys Leu His Ser Leu	745	750	755	
tca act cta tct aga aac aag aac tat gtc cgt ccc gag ttt gtg gat				2418
Ser Thr Leu Ser Arg Asn Lys Asn Tyr Val Arg Pro Glu Phe Val Asp	760	765	770	
gac tgt gaa cca gtt gag ata aac ata cag tct ggt cgt cat cct gta				2466
Asp Cys Glu Pro Val Glu Ile Asn Ile Gln Ser Gly Arg His Pro Val	775	780	785	
ctg gag act ata tta caa gat aac ttc gtc cca aat gac aca att ttg				2514
Leu Glu Thr Ile Leu Gln Asp Asn Phe Val Pro Asn Asp Thr Ile Leu	795	800	805	
cat gca gaa ggg gaa tat tgc caa att atc acc gga cct aac atg gga				2562
His Ala Glu Gly Glu Tyr Cys Gln Ile Ile Thr Gly Pro Asn Met Gly	810	815	820	
gga aag agc tgc tat atc cgt caa gtt gct tta att tcc ata atg gct				2610
Gly Lys Ser Cys Tyr Ile Arg Gln Val Ala Leu Ile Ser Ile Met Ala	825	830	835	
cag gtt ggt tcc ttt gta cca gcg tca ttc gcc aag ctg cac gtg ctt				2658
Gln Val Gly Ser Phe Val Pro Ala Ser Phe Ala Lys Leu His Val Leu	840	845	850	
gat ggt gtt ttc act cgg atg ggt gct tca gac agt atc cag cat ggc				2706
Asp Gly Val Phe Thr Arg Met Gly Ala Ser Asp Ser Ile Gln His Gly	855	860	865	
aga agt acc ttt cta gaa gaa tta agt gaa gcg tca cac ata atc aga				2754
Arg Ser Thr Phe Leu Glu Glu Leu Ser Glu Ala Ser His Ile Ile Arg	870	875	880	885
acc tgt tct tct cgt tcg ctt gtt ata tta gat gag ctt gga aga ggc				2802
Thr Cys Ser Ser Arg Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly	890	895	900	
act agc aca cac gac ggt gta gcc att gcc tat gca aca tta cag cat				2850
Thr Ser Thr His Asp Gly Val Ala Ile Ala Tyr Ala Thr Leu Gln His	905	910	915	
ctc cta gca gaa aag aga tgt ttg gtt ctt ttt gtc acg cat tac cct				2898
Leu Leu Ala Glu Lys Arg Cys Leu Val Leu Phe Val Thr His Tyr Pro	920	925	930	
gaa ata gct gag atc agt aac gga ttc cca ggt tct gtt ggg aca tac				2946
Glu Ile Ala Glu Ile Ser Asn Gly Phe Pro Gly Ser Val Gly Thr Tyr	935	940	945	

50		55		60
Leu Ser Pro His Thr	Gln Asn Pro Val Pro Asp	Pro Asn Leu His Gln		
65	70	75	80	
Arg Phe Leu Gln Arg	Phe Leu Glu Pro Ser	Pro Glu Glu Tyr Val Pro		
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Glu Thr Ser Ser Arg	Lys Tyr Thr Pro	Leu Glu Gln Gln Val Val		
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Glu Leu Lys Ser Lys	Tyr Pro Asp Val Val	Leu Met Val Glu Val Gly		
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Tyr Arg Tyr Arg Phe	Phe Gly Glu Asp Ala	Glu Ile Ala Ala Arg Val		
	130	135	140	
Leu Gly Ile Tyr Ala	His Met Asp His Asn	Phe Met Thr Ala Ser Val		
145	150	155	160	
Pro Thr Phe Arg Leu	Asn Phe His Val Arg	Arg Leu Val Asn Ala Gly		
	165	170	175	
Tyr Lys Ile Gly Val	Val Lys Gln Thr Glu	Thr Ala Ala Ile Lys Ser		
	180	185	190	
His Gly Ala Asn Arg	Thr Gly Pro Phe Phe	Arg Gly Leu Ser Ala Leu		
	195	200	205	
Tyr Thr Lys Ala Thr	Leu Glu Ala Ala Glu	Asp Ile Ser Gly Gly Cys		
	210	215	220	
Gly Gly Glu Glu Gly	Phe Gly Ser Gln Ser	Asn Phe Leu Val Cys Val		
225	230	235	240	
Val Asp Glu Arg Val	Lys Ser Glu Thr Leu	Gly Cys Gly Ile Glu Met		
	245	250	255	
Ser Phe Asp Val Arg	Val Gly Val Val Gly	Val Glu Ile Ser Thr Gly		
	260	265	270	
Glu Val Val Tyr Glu	Glu Phe Asn Asp Asn	Phe Met Arg Ser Gly Leu		
	275	280	285	
Glu Ala Val Ile Leu	Ser Leu Ser Pro Ala	Glu Leu Leu Leu Gly Gln		
	290	295	300	
Pro Leu Ser Gln Gln	Thr Glu Lys Phe Leu	Val Ala Met Ala Gly Pro		
305	310	315	320	
Thr Ser Asn Val Arg	Val Glu Arg Ala Ser	Leu Asp Cys Phe Ser Asn		
	325	330	335	
Gly Asn Ala Val Asp	Glu Val Ile Ser Leu	Cys Glu Lys Ile Ser Ala		
	340	345	350	
Gly Asn Leu Glu Asp	Asp Lys Glu Met Lys	Leu Glu Ala Ala Glu Lys		
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Gly Met Ser Cys Leu	Thr Val His Thr Ile	Met Asn Met Pro His Leu		
	370	375	380	
Thr Val Gln Ala Leu	Ala Leu Thr Phe Cys	His Leu Lys Gln Phe Gly		
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Phe Glu Arg Ile Leu	Tyr Gln Gly Ala Ser	Phe Arg Ser Leu Ser Ser		
	405	410	415	
Asn Thr Glu Met Thr	Leu Ser Ala Asn Thr	Leu Gln Gln Leu Glu Val		
	420	425	430	
Val Lys Asn Asn Ser	Asp Gly Ser Glu Ser	Gly Ser Leu Phe His Asn		
	435	440	445	
Met Asn His Thr Leu	Thr Val Tyr Gly Ser	Arg Leu Leu Arg His Trp		
	450	455	460	
Val Thr His Pro Leu	Cys Asp Arg Asn Leu	Ile Ser Ala Arg Leu Asp		
465	470	475	480	
Ala Val Ser Glu Ile	Ser Ala Cys Met Gly	Ser His Ser Ser Ser Gln		
	485	490	495	
Leu Ser Ser Glu Leu	Val Glu Glu Gly Ser	Glu Arg Ala Ile Val Ser		
	500	505	510	

Pro	Glu	Phe	Tyr	Leu	Val	Leu	Ser	Ser	Val	Leu	Thr	Ala	Met	Ser	Arg	515	520	525
Ser	Ser	Asp	Ile	Gln	Arg	Gly	Ile	Thr	Arg	Ile	Phe	His	Arg	Thr	Ala	530	535	540
Lys	Ala	Thr	Glu	Phe	Ile	Ala	Val	Met	Glu	Ala	Ile	Leu	Leu	Ala	Gly	545	550	555
Lys	Gln	Ile	Gln	Arg	Leu	Gly	Ile	Lys	Gln	Asp	Ser	Glu	Met	Arg	Ser	565	570	575
Met	Gln	Ser	Ala	Thr	Val	Arg	Ser	Thr	Leu	Leu	Arg	Lys	Leu	Ile	Ser	580	585	590
Val	Ile	Ser	Ser	Pro	Val	Val	Val	Asp	Asn	Ala	Gly	Lys	Leu	Leu	Ser	595	600	605
Ala	Leu	Asn	Lys	Glu	Ala	Ala	Val	Arg	Gly	Asp	Leu	Leu	Asp	Ile	Leu	610	615	620
Ile	Thr	Ser	Ser	Asp	Gln	Phe	Pro	Glu	Leu	Ala	Glu	Ala	Arg	Gln	Ala	625	630	635
Val	Leu	Val	Ile	Arg	Glu	Lys	Leu	Asp	Ser	Ser	Ile	Ala	Ser	Phe	Arg	645	650	655
Lys	Lys	Leu	Ala	Ile	Arg	Asn	Leu	Glu	Phe	Leu	Gln	Val	Ser	Gly	Ile	660	665	670
Thr	His	Leu	Ile	Glu	Leu	Pro	Val	Asp	Ser	Lys	Val	Pro	His	Asn	Trp	675	680	685
Val	Lys	Val	Asn	Ser	Thr	Lys	Lys	Thr	Ile	Arg	Tyr	His	Pro	Pro	Glu	690	695	700
Ile	Val	Ala	Gly	Leu	Asp	Glu	Leu	Ala	Leu	Ala	Thr	Glu	His	Leu	Ala	705	710	715
Ile	Val	Asn	Arg	Ala	Ser	Trp	Asp	Ser	Phe	Leu	Lys	Ser	Phe	Ser	Arg	725	730	735
Tyr	Tyr	Thr	Asp	Phe	Lys	Ala	Ala	Val	Gln	Ala	Leu	Ala	Ala	Leu	Asp	740	745	750
Cys	Leu	His	Ser	Leu	Ser	Thr	Leu	Ser	Arg	Asn	Lys	Asn	Tyr	Val	Arg	755	760	765
Pro	Glu	Phe	Val	Asp	Asp	Cys	Glu	Pro	Val	Glu	Ile	Asn	Ile	Gln	Ser	770	775	780
Gly	Arg	His	Pro	Val	Leu	Glu	Thr	Ile	Leu	Gln	Asp	Asn	Phe	Val	Pro	785	790	795
Asn	Asp	Thr	Ile	Leu	His	Ala	Glu	Gly	Glu	Tyr	Cys	Gln	Ile	Ile	Thr	805	810	815
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Ile	Ser	Ile	Met	Ala	Gln	Val	Gly	Ser	Phe	Val	Pro	Ala	Ser	Phe	Ala	835	840	845
Lys	Leu	His	Val	Leu	Asp	Gly	Val	Phe	Thr	Arg	Met	Gly	Ala	Ser	Asp	850	855	860
Ser	Ile	Gln	His	Gly	Arg	Ser	Thr	Phe	Leu	Glu	Glu	Leu	Ser	Glu	Ala	865	870	875
Ser	His	Ile	Ile	Arg	Thr	Cys	Ser	Ser	Arg	Ser	Leu	Val	Ile	Leu	Asp	885	890	895
Glu	Leu	Gly	Arg	Gly	Thr	Ser	Thr	His	Asp	Gly	Val	Ala	Ile	Ala	Tyr	900	905	910
Ala	Thr	Leu	Gln	His	Leu	Leu	Ala	Glu	Lys	Arg	Cys	Leu	Val	Leu	Phe	915	920	925
Val	Thr	His	Tyr	Pro	Glu	Ile	Ala	Glu	Ile	Ser	Asn	Gly	Phe	Pro	Gly	930	935	940
Ser	Val	Gly	Thr	Tyr	His	Val	Ser	Tyr	Leu	Thr	Leu	Gln	Lys	Asp	Lys	945	950	955
Gly	Ser	Tyr	Asp	His	Asp	Asp	Val	Thr	Tyr	Leu	Tyr	Lys	Leu	Val	Arg	960		

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Gly	Leu	Cys	Ser	Arg	Ser	Phe	Gly	Phe	Lys	Val	Ala	Gln	Leu	Ala	Gln				
			980						985					990					
Ile	Pro	Pro	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ser	Met	Ala	Ala	Lys	Leu				
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Glu	Ala	Glu	Val	Arg	Ala	Arg	Glu	Arg	Asn	Thr	Arg	Met	Gly	Glu	Pro				
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Glu	Gly	His	Glu	Glu	Pro	Arg	Gly	Ala	Glu	Glu	Ser	Ile	Ser	Ala	Leu				
1025					1030					1035					1040				
Gly	Asp	Leu	Phe	Ala	Asp	Leu	Lys	Phe	Ala	Leu	Ser	Glu	Glu	Asp	Pro				
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Trp	Lys	Ala	Phe	Glu	Phe	Leu	Lys	His	Ala	Trp	Lys	Ile	Ala	Gly	Lys				
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 <213> Artificial Sequence

<220>
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<210> 21
 <211> 28
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<220>
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<210> 22
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<220>
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<210> 23
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<210> 24
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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<210> 25
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 26
<211> 2188
<212> DNA
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<223> Clone 43

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ccgtctggat ttaagccggc tgaatccgcc ggtgatgctt cgtccctgtt ctccaatatt 300
atgcataagt ttgtaaaagt cgatgatcga gattgttctg gagagaggag ccgagaagat 360
gttgttccgc tgaatgattc atctctatgt atgaaggcta atgatgttat tcctcaattt 420
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gaggataagg ttctgtgatt ggactctaac aaaaggctga aaatgctcca ggatccgggt 660
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atcagggatg ccaatagaag acgtcctgat gatccccctt acgatagaaa gaccttacac 780
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<211> 1385

<212> DNA

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<223> Clone 62

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aggaatcaaa tatgatgagt ttgctttata aactctgtaa acttcctata ttagtaggaa 180
aaagcgggct agagttattt ctttctcaat tccaagcagc catagatagc gactttccaa 240
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<210> 28
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<212> DNA
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<220>
<223> MSH6 specific primer 2S8 for PCR using cDNA of
Arabidopsis thaliana ecotype Columbia.

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<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> MSH6 specific primer S82 for PCR using cDNA of
Arabidopsis thaliana ecotype Columbia.

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<210> 30
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tctctctcac aattccaaaa a atg cag cgc cag aga tcg att ttg tct ttc 171
Met Gln Arg Gln Arg Ser Ile Leu Ser Phe
1 5 10

ttc caa aaa ccc acc gcg gcg act acg aag ggt ttg gtt tcc ggc gat 219
Phe Gln Lys Pro Thr Ala Ala Thr Thr Lys Gly Leu Val Ser Gly Asp
15 20 25

gct gct agc ggc ggg ggc ggc agc gga gga cca cga ttt aat gtg aag 267
Ala Ala Ser Gly Gly Gly Gly Ser Gly Gly Pro Arg Phe Asn Val Arg
30 35 40

gaa ggg gat gct aaa ggc gac gct tct gta cgt ttt gct gtt tcg aaa 315
Glu Gly Asp Ala Lys Gly Asp Ala Ser Val Arg Phe Ala Val Ser Lys
45 50 55

tct gtc gat gag gtt aga gga acg gat act cca ccg gag aag gtt ccg	363
Ser Val Asp Glu Val Arg Gly Thr Asp Thr Pro Pro Glu Lys Val Pro	
60 65 70	
cggt cgt gtc ctg ccg tct gga ttt aag ccg gct gaa tcc gcc gst gat	411
Arg Arg Val Leu Pro Ser Gly Phe Lys Pro Ala Glu Ser Ala Gly Asp	
75 80 85 90	
gct tcg tcc ctg ttc tcc aat att atg cat aag ttt gta aaa gtc gat	459
Ala Ser Ser Leu Phe Ser Asn Ile Met His Lys Phe Val Lys Val Asp	
95 100 105	
gat cga gat tgt tct gga gag agg agc cga gaa gat gtt gtt ccg ctg	507
Asp Arg Asp Cys Ser Gly Glu Arg Ser Arg Glu Asp Val Val Pro Leu	
110 115 120	
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Asn Asp Ser Ser Leu Cys Met Lys Ala Asn Asp Val Ile Pro Gln Phe	
125 130 135	
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Arg Ser Asn Asn Gly Lys Thr Gln Glu Arg Asn His Ala Phe Ser Phe	
140 145 150	
agt ggg aga gct gaa ctt aga tca gta gaa gat ata gga gta gat ggc	651
Ser Gly Arg Ala Glu Leu Arg Ser Val Glu Asp Ile Gly Val Asp Gly	
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Asp Val Pro Gly Pro Glu Thr Pro Gly Met Arg Pro Arg Ala Ser Arg	
175 180 185	
ttg aag cga gtt ctg gag gat gaa atg act ttt aag gag gat aag gtt	747
Leu Lys Arg Val Leu Glu Asp Glu Met Thr Phe Lys Glu Asp Lys Val	
190 195 200	
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Pro Val Leu Asp Ser Asn Lys Arg Leu Lys Met Leu Gln Asp Pro Val	
205 210 215	
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Cys Gly Glu Lys Lys Glu Val Asn Glu Gly Thr Lys Phe Glu Trp Leu	
220 225 230	
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Glu Ser Ser Arg Ile Arg Asp Ala Asn Arg Arg Arg Pro Asp Asp Pro	
235 240 245 250	
ctt tac gat aga aag acc tta cac ata cca cct gat gtt ttc aag aaa	939
Leu Tyr Asp Arg Lys Thr Leu His Ile Pro Pro Asp Val Phe Lys Lys	
255 260 265	
atg tct gca tca caa aag caa tat tgg agt gtt aag agt gaa tat atg	987
Met Ser Ala Ser Gln Lys Gln Tyr Trp Ser Val Lys Ser Glu Tyr Met	
270 275 280	
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Asp	Ile	Val	Leu	Phe	Phe	Lys	Val	Gly	Lys	Phe	Tyr	Glu	Leu	Tyr	Glu	
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cta	gat	gcg	gaa	tta	ggc	cac	aag	gag	ctt	gac	tgg	aag	atg	acc	atg	1083
Leu	Asp	Ala	Glu	Leu	Gly	His	Lys	Glu	Leu	Asp	Trp	Lys	Met	Thr	Met	
	300					305				310						
agt	ggc	gtg	gga	aaa	tgc	aga	cag	gtt	ggc	atc	tct	gaa	agt	ggg	ata	1131
Ser	Gly	Val	Gly	Lys	Cys	Arg	Gln	Val	Gly	Ile	Ser	Glu	Ser	Gly	Ile	
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Asp	Glu	Ala	Val	Gln	Lys	Leu	Leu	Ala	Arg	Gly	Tyr	Lys	Val	Gly	Arg	
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Ser	Glu	Gly	Asn	Ile	Gly	Pro	Asp	Ala	Val	His	Leu	Leu	Ala	Ile	Lys	
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	395				400					405					410	
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Phe	Val	Asp	Cys	Ala	Ala	Leu	Arg	Phe	Trp	Val	Gly	Ser	Ile	Ser	Asp	
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gat	gca	tca	tgt	gct	gct	ctt	gga	gcg	tta	ttg	atg	cag	gtt	tct	cca	1467
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Pro	Val	Pro	Gln	Val	Met	Gly	Asp	Thr	Asp	Ala	Ala	Gly	Val	Arg	Asn	
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Ile	Ile	Glu	Ser	Asn	Gly	Tyr	Phe	Lys	Gly	Ser	Ser	Glu	Ser	Trp	Asn	
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Cys	Ala	Val	Asp	Gly	Leu	Asn	Glu	Cys	Asp	Val	Ala	Leu	Ser	Ala	Leu	

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Gly	Glu	Leu	Ile	Asn	His	Leu	Ser	Arg	Leu	Lys	Leu	Glu	Asp	Val	Leu	
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Lys	His	Gly	Asp	Ile	Phe	Pro	Tyr	Gln	Val	Tyr	Arg	Gly	Cys	Leu	Arg	
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Ile	Asp	Gly	Gln	Thr	Met	Val	Asn	Leu	Glu	Ile	Phe	Asn	Asn	Ser	Cys	
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Ile	Asp	Leu	Leu	Leu	Ala	Leu	Gln	Lys	Glu	Ser	Asn	Met	Met	Ser	Leu	
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Glu	Leu	Phe	Leu	Ser	Gln	Phe	Glu	Ala	Ala	Ile	Asp	Ser	Asp	Phe	Pro	
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Asn	Tyr	Gln	Asn	Gln	Asp	Val	Thr	Asp	Glu	Asn	Ala	Glu	Thr	Leu	Thr	
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Ile His Thr Ile Ser Cys Leu Asp Val Leu Arg Ser Phe Ala Ile Ala	
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Ser Glu Ala Thr Asp Gln Asn Gln Lys Thr Lys Gly Pro Ile Leu Lys	
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Ile Gln Gly Leu Trp His Pro Phe Ala Val Ala Ala Asp Gly Gln Leu	
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Pro Val Pro Asn Asp Ile Leu Leu Gly Glu Ala Arg Arg Ser Ser Gly	
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Ser Ile His Pro Arg Ser Leu Leu Leu Thr Gly Pro Asn Met Gly Gly	
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Lys Ser Thr Leu Leu Arg Ala Thr Cys Leu Ala Val Ile Phe Ala Gln	
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Leu Gly Cys Tyr Val Pro Cys Glu Ser Cys Glu Ile Ser Leu Val Asp	
875 880 885 890	
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Thr Ile Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met Thr Gly Glu	
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Val Glu Lys Val Gln Cys Arg Met Leu Phe Ala Thr His Tyr His Pro	
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Leu Thr Lys Glu Phe Ala Ser His Pro Arg Val Thr Ser Lys His Met
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gct tgc gca ttc aaa tca aga tct gat tat caa cca cgt ggt tgt gat 3147
Ala Cys Ala Phe Lys Ser Arg Ser Asp Tyr Gln Pro Arg Gly Cys Asp
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caa gac cta gtg ttc ttg tac cgt tta acc gag gga gct tgt cct gag 3195
Gln Asp Leu Val Phe Leu Tyr Arg Leu Thr Glu Gly Ala Cys Pro Glu
          1005                      1010                      1015

agc tac gga ctt caa gtg gca ctc atg gct gga ata cca aac caa gtg 3243
Ser Tyr Gly Leu Gln Val Ala Leu Met Ala Gly Ile Pro Asn Gln Val
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gtt gaa aca gca tca ggt gct gct caa gcc atg aag aga tca att ggg 3291
Val Glu Thr Ala Ser Gly Ala Ala Gln Ala Met Lys Arg Ser Ile Gly
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Glu Asn Phe Lys Ser Ser Glu Leu Arg Ser Glu Phe Ser Ser Leu His
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His Glu Ile Lys Ser Ser Tyr Cys Val Pro Lys
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Arg	Ser	Val	Glu	Asp	Ile	Gly	Val	Asp	Gly	Asp	Val	Pro	Gly	Pro	Glu
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Thr	Pro	Gly	Met	Arg	Pro	Arg	Ala	Ser	Arg	Leu	Lys	Arg	Val	Leu	Glu
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 <211> 22
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 SSLP marker in Arabidopsis thaliana subspecies.

 <400> 47
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 <210> 48
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 <220>
 <223> Forward primer for PCR amplification of NGA128
 SSLP marker in Arabidopsis thaliana subspecies.

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 <210> 49
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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

<400> 49
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<210> 50
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 53
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<210> 54
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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 <210> 61
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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 <210> 63
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

<400> 68
 gaaaaaacgc tactttcgtg g 21

<210> 69
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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

<400> 69
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<210> 70
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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 71
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 SSLP marker in Arabidopsis thaliana subspecies.

<400> 71
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<210> 72
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 marker in Arabidopsis thaliana subspecies.

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<210> 73
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 <220>
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 marker in *Arabidopsis thaliana* subspecies.

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 <210> 74
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 marker in *Arabidopsis thaliana* subspecies.

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 <210> 75
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 marker in *Arabidopsis thaliana* subspecies.

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 <210> 76
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 <223> Forward primer for PCR amplification of NGA8 SSLP
 marker in *Arabidopsis thaliana* subspecies.

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 <210> 77
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 <220>
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 marker in *Arabidopsis thaliana* subspecies.

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<210> 78
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 <220>
 <223> Forward primer for PCR amplification of NGA1107
 SSLP marker in Arabidopsis thaliana subspecies.

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 <210> 79
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 <220>
 <223> Reverse primer for PCR amplification of NGA1107
 SSLP marker in Arabidopsis thaliana subspecies.

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 <210> 80
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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 <223> Forward primer for PCR amplification of NGA249
 SSLP marker in Arabidopsis thaliana subspecies.

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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 89
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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 90
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 <223> Forward primer for PCR amplification of NGA139
 SSLP marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 92
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<212> DNA
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 marker in Arabidopsis thaliana subspecies.

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<210> 93
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<220>
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 marker in Arabidopsis thaliana subspecies.

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 SSLP marker in Arabidopsis thaliana subspecies.

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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

<400> 95
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<210> 96
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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 97
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<220>
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 SSLP marker in Arabidopsis thaliana subspecies.

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<210> 99

<211> 1047

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 99

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Gln Pro Thr Ile Ser Arg Phe Phe Lys Lys Ala Val Lys Ser Glu Leu

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Ser	Asp	Gly	Arg	Ile	Gly	Lys	Gln	Ser	Pro	Leu	Leu	Phe	Arg	Leu	Phe	580	585	590
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<210> 100

<211> 1242

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 100

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Ser	Asp	Ile	Met	His	Ser	Gln	Glu	Pro	Gln	Ser	Asp	Thr	Met	Leu	Asn
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